

In the Specification

Please substitute the following pages 29 through 60 with the attached pages 29 through 66.

Table 1. Differentially expressed genes in LGL1 and LGL2. This data is based on Incyte Genomics and Affymetrix Chip FL 6800				
	Incyte Genomics		Affymetrix	
Gene Name	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
Upregulated Genes				
<i>Proteolytic enzymes</i>				
Granzyme H precursor	6.3 (3332/533)	M57888 NM033423 BC027974	(1.5/1.8) (21.8/10.8)	M37245 M28879
Lymphopain (Cathepsin CathapsinW)	5.4 (3578/658)	AF013661 NM001335 BC035637 BC048255	_____	
Perforin	3.8 (1549/413)	L40557 BC063043 X13224 X12940 M28393	(103-44.7)	M31951
Matrix metalloprotease metalloprotenase 8 (neutrophil collagenase)	3.2 (1178/370)	J05556 NM002424	(1.0/-1.1)	
Calpain, small polypeptide	2.0 (4089/2059)	X04106 BC064998 BC023643 BC017308 NM001749 BC018931 BC000592 BC011903 BC007779 BC021933 BT009775 NM032330 BC006000 BC005397 AY052551	(1.1/1.3)	

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Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
Granzyme A	1.9 (1944/1022)	NM06144 BC015739	_____	
Caspase 8 (From RPA also)	1.4 (2035/1480)	U97075 NM033357 NM033358	(1.2/-1.4)	AF005775
<i>Inducible or regulated proteins</i>				
Interferon regulated factor 4	5.0 (1128/226)	U52682	(6/-1.5)	
TNF- α induced protein A 20	3.2 (1507/470)	M59465	(-1.3/-3.8)	
Heat shock 70 let kd protein 5 (Glucose regulated protein 78 kd)	2.8 (4090/1464)	X87949	(5.3/14.5)	M11717
RANTES (RPA also)	2.7 (2490/909)	M21121	(5.9/6)	
Human rap 2 mRNA for ras related protein proteins	2.6 (899/327)	X12534	_____	
p53 inducible proteins	2.2 (2040/916)	L47738	(2.9/2.3)	
Glucose regulated proteins 58 kd receptors	2.2 (3661/1641)	AL043206	_____	
RECEPTORS				
CD8 antigen, alpha polypeptide (p32)	7.3 (4325/594)	M12824	(-1.2/-1.1)	M27161

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Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
Killer cell lectin-like receptor subfamily C, member 2 (NKG2-CII)	5.5 (2115/383)	AJ001684		
CD8 antigen beta polypeptide (p37)	9.0 (1953/401)	NM004931	(7.2/5.2)	X13444
Musculin (activated B-cell factor-1)	4.1 (466/113)	AF087036		
Killer cell lectin-like receptor subfamily C, member 3 (NKG2-CII)	3.8 (1335/344)	AJ001685		
subfamily C, member 2 (NKG2-CII)	5.5 (2115/383)	AJ001684		
CD8 antigen beta polypeptide (p37)	4.9 (1953/401)	X13444	(7.2/5.2)	
Musculin (activated B-cell factor-1) Killer cell lectin-like receptor	4.1 (466/113)	AF060154		
Low affinity immunoglobulin Gamma FC receptor III-1 precursor	3.9 (1335/344)	J04162	(8.1/6.8)	
Filamin I (actin-binding protein-280)	3.8 (1085/287)	X53416	(2.1/1.9)	

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Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
Lectin-like Type II integral Membrane protein (NKG2-E)	3.8 (1300/344)	AJ001685		
Natural Killer cells group 7	3.1 (11251/3591)	S69115	(9.3/9.1)	
Protein tyrosine phosphatase type J receptor	2.1 (4614/2177)	L05148	(2.9/2.6)	
Delta sleep inducing peptide Immunoreceptor	2.3 (5424/2319)	BE295817		
Lymphotoxin-Beta receptor precursor	2.3 (3587/1544)	AI271415		
MHC class II, DR beta 5 receptor	2.4 (2264/953)	X00700		
NKG2-D type II integral membrane protein	2.1 (1019/494)	X54870	(7.3/9.4)	
Protein tyrosine phosphatase Non-receptor type 12	2.1 (1036/494)	M93425	(1.6/1.0)	
Leukemia virus receptor (CGLVR1)	2.1 (713/340)	L20859	(2.9/2.5)	

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Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
<i>Kinases and Phosphatases</i>				
Dual specificity Phosphatase-1 (PAC-1)	4.2 (2484/585)	L11329	(1.6/1.2)	
Dual specificity Phosphatase-5	2.7 (857/320)	U10886	(1.1/1.6)	
Tyrosine protein tyrosine phosphatase	2.6 (713/272)	U15932	(1.2/2.3)	
Protein Kinase C etc	2.2 (2780/1239)	M55284	————	
Zeta Chain (TCR) associated protein kinase (70kd)	2.1 (4614/2177)	L05148	(2.9/2.6)	
Src Kinase-associated phosphoprotein of 55kd	2.1 (730/327)	Y11215	(3.3/2.4)	
Phosphatidyl inositol (4,5,bisphosphatase5-phosphatase homolog	2.1 (764/372)	638789	————	
Protein phosphatase 2. Regulated subunit B (B56)	2.0 (1071/526)	U37352	(6.8/5.8)	
Protein Phosphatase 1, (catalytic subunit, alpha isoform)	2.0 (1643/835)	J04759		

Table 1. Differentially expressed genes in LGL1 and LGL2. This data is based on Incyte Genomics and Affymetrix Chip FL 6800

Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
<i>Transcription Factors</i>				
Runt related transcription factors 3	3.5 (2689/775)	D43968	(3.8/3.5)	
<i>Miscellaneous</i>				
EST.1	17.7 (346/189)	H06366		
EST.2	11.8 (2571/218)	AA482549		
EST.3	3.0 (544/182)	N47089		
Solute carrier protein	4.6 (785/172)	L14595	(1.4/1.6)	
Filamin A alpha	3.8 (1085/287)	X53416	(2.1/1.9)	
Hemoglobin delta	3.1 (2084/667)	V00505		
Hemoglobin beta	3.0 (4319/1419)	V00497		
KIAA 0668 protein	2.6 (3476/1254)	AB014568		
MHC, Class II DR beta 3	2.4 (2264/953)	X00700		
PLECKSTRIN	2.4 (2033/854)	X07743	(2.0/2.4)	
Isocitrate dehydrogenase 2 (NADP+) Mitochondrial	2.2 (2067/893)	X69433	(2.2/2.7)	
Putative translation initiation factor	2.0 (4003/2046)	L26247	(-1.3/-1.5)	

Table 1. Differentially expressed genes in LGL1 and LGL2. This data is based on Incyte Genomics and Affymetrix Chip FL 6800

Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
Tubulin, Beta polypeptide	2.0 (2640/1349)	AW163523		
Ubiquitin B	1.9 (5668/3024)	BE250544		
Moesin	1.8 (5015/2750)	Z98946		
Nuclear factor of activated T cells, cytoplasmic	1.8 (2586/1440)	U85430	(1.8/2.9)	
Ubiquitin C	1.7 (3568/2071)	AA600188		
GTP binding protein, alpha 13	1.8 (2147/1195)	U87964	(-1.3/-1.5)	
Calritculin Calritculin Precursor	2.2 (3101/1384)	M84739	(2.0/2.2)	
KIAA0158 gene complete CDs	3.9 (2953/753)	063878		
Hemoglobin alpha I	3.2 (1074/333)	V00491		
T cell receptor gamma chain	3.1 (987/315)	M30894	(5.0/11.3)	
FYN Oncogene related to SRC FGR, YES	3.x (3405/313)	Z97989		
EB1 mRNA	2.4 (1075/442)	U24166	(-1.8/-2)	
PLECKSTRIN	2.4 (2033/854)	X07743		

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Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
DNAJ protein Homolog	2.4 (237/1065)	D85429	(1.4/-1.7)	
MHC Class II HLA-DRW 10 beta	2.4 (2264/953)	D85429		
Lymphotoxin-beta receptor precursor	2.3 (3587/1544)	L04270		
Leucine Zipper Protein	2.3 (5424/2319)	50781 <u>Z50781</u>	(1.4/-2.7)	
Probable protein disulfide Isomerase ER-60 precursor	2.2 (3661/1641)	Z49835	(1.4/1.0)	
Troponin T, Fast skeletal muscle Isomerase beta	2.2 (1628/743)	M21984		
Transforming growth factor receptor III	3.7 (764/204)	L07594	(10.6/7.1)	
DEC1, complete cds	3.5 (1498/1429)	AB004066		
Granulocyte Colony-stimulating Factor induced gene	3.1 (11251/3591)	S65115	(9.3/9.1)	
Integrin, beta 2	2.7 (3718/1377)	M15395		
Clone 23912	2.6 (3476/1341)	AF038178		
Putative tumor suppressor Protein (RDA32)	2.5 (1145/453)	AF061836		

Table 1. Differentially expressed genes in LGL1 and LGL2. This data is based on Incyte Genomics and Affymetrix Chip FL 6800

Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
Down regulated genes				
Homo sapiens Indian hedgehog protein (IHH)	-18.6 (477/7779)	L38517	(-1.6/-1.1)	
CD20 Receptor	-16.2 (229/3703)	X07203	(1.1/-1.9)	
Human germline IgD chain gene, C-region	-11.0 (210/2313)	K02882	(-9.5/-7.5)	
Human transporter Protein (g17)	-10.4 (300/3124)	U49082	(-2/-1)	
Ribosomal protein S26	-6.2 (321/1853)	X69654	(-3.1/1.1)	
EST	-3.4 (429/1371)	R85437		
CD 72 antigen	-3.3 (353/1165)	M54992	(1.3/1.7)	
EST	-2.5 (629/1583)	AA916867		
Endothelial differentiation protein (Edg-1)	-2.5 (447/1033)	M31210	(-2.6/-5.2)	
Diacylglycerol kinase, alpha (80kD)	-2.5 (883/2172)	X62535	(-1.4/-2.3)	
60S Ribosomal protein L41	-2.3 (5372/2339)	Z12962	(-1.2/-1.2)	

Table 1. Differentially expressed genes in LGL1 and LGL2. This data is based on Incyte Genomics and Affymetrix Chip FL 6800

Gene Name	Incyte Genomics		Affymetrix	
	BDE (p1/p2)	GenBankID	Fold Change (LGL1/LGL2)	GenBank ID If different from Incyte Genomics
EST	-2.3 (708/1616)	AA134589		

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
perforin	32904_at	72.8	39.5	45.4	8.5
serine protease	40078_at	55.7	48.7	38.7	3.0
mast cell function-associated antigen homolog (MAFA)	34975_at	66.2 <u>55.2</u>	45.4	61.1	16.2
NK-receptor (NK-p46)	34039_at	53.6	45.2	50.6	7.8
gb=W28589	40913_at	47.7	41.2	44.2	23.9
suppressor related (DOC-1R)	35151_at	45.3	40.1	27.0	42.8
ribosomal protein S6 kinase 1 (RPS6KA1)	1127_at	42.4	40.0	50.6	2.2
butyrophillin (BT3.3)	38759_at	37.8	33.3	52.9	17.8
CD94	33531_at	35.2	34.2	17.9	7.3
MEGF9	36488_at	34.1	44.8 <u>44.6</u>	33.4	10.3
chronic granulomatous disease protein	40159_r_at	33.7	83.5	63.5	8.8
gamma2-adaptin (G2AD)	38799_at	30.3	29.2	27.5	40.5
calcineurin A2	39780_at	29.0	17.4	15.2	19.0
beta adaptin	35181 <u>36161</u> _at	26.4 <u>28.4</u>	21.1	11.5	26.7
G protein-coupled receptor V28	40646_at	27.4	40.3	25.1	5.1
thrombin receptor	41700_at	22.5	8.3	14.2	4.8
GTPase-activating protein	36846 <u>36843</u> _at	22.1	9.1	19.5	12.2
SH3 domain containing adaptor protein (SCAP(SCAP))	34432_at	21.9	10.4	22.8	10.3
AML1c	39421_at	21.5 <u>21.8</u>	17.2	31.7	10.6

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
KIAA0664 protein	34259_at	21.7	38.4	27.0	18.0
gb=AA978353	41126_at	21.4	8.8	13.9	1.4
Metk Matk=megakaryocyte-associated tyrosine kinase	36264_at	20.7	17.1	13.1	1.4
vascular smooth-muscle alpha-actin	32755_at	20.1	27.8	22.0	3.8
lysyl hydroxylase (PLOD)	36184_at	19.8	18.0	9.8	1.1
candidate tumor suppressor gene 21 protein isoform 4I	40497_at	19.7	16.1	26.6	13.1
beta2-syntrophin (SNT B2)	40589_at	19.2	22.3	22.1	13.1
hexokinase III (HK3)	38372 36372_at	18.8	39.6	4.1	6.7
telomeric repeat DNA-binding protein (PIN2)	1329_s_at	17.3	12.9	14.3	13.8
cytotoxic T-lymphocyte-associated serine esterase 1 (CTLA1)	32370_at	17.3	12.1	9.8	1.6
T cell-specific cell-specific protein (RANTES)	1404_r_at	17	10.2	18.3	4.5
CMRF-35-H9	41059_at	16.8	21.0	15.6	5.7
human-Human immune interferon (IFN-gamma)	1021_at	16.7	21.7	18.8	-2.1
placenta (Diff48)	32978_g_at	16.5	14.4	6.9	23.7
medium-chain acyl-CoA dehydrogenase (MCAD)	37532_at	16.4	15.1	18.6	28.3
mRNA for Y3K+YSK1	40104_at	16.3	12.5	13.2	19.1
m3A-m6A methyltransferase (MT-A70)	32245_at	16.2	16.4	19.8	27.4
CD3G gene, exon 1	39228 39226_at	16.2	6	5.3	3.4
PUTATIVE PUTATIVE novel protein similar to many (archaeal) bacterial, worm and yeast hypothetical proteins	41249_at	15.6 15.8	27.6	27.5	8.2

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=A1004207 <u>A1004207</u>	36732_at	15.8	25.1	17.6	22.2
microsomal glutathione glutathione S-transferase (3- MGST3)3-(MGST3)	39018_at	15.6	21.8	16.9	28.4
similar to mouse mouse Choline/Ethanolamine Ethanolamine Kinase (O55229)	32033_at	15.6	14.4	13.5 <u>13.6</u>	25.3
25S-26S proteasome subunit p40.5	32211_at	15.3	15.2	11.7	12.7
FeFc -gamma RIII-1	31499-at <u>s_at</u>	15	5.8	5.4	-4.1
gb=AF070644	3885238652 at	14.6	16.6	14.4	8.4
gb=U79260	37242_at	14.5	15.9	11.5	17.5
Ste=20 related kinase SPAK	40986_at	14.5	10.9	18.2	8.2
guanine Guanine Nucleotide-Binding Protein Rap2	1819_at	14.5	5.8	6.5	4.1
SCA1 mRNA for ataxin	3814236142 at	14.2	13.2	16.9	7.7
butyrophillin butyrophilin (BTF4)	38760-at_f_at	14.2	13.3	18.7	7.1
HBV associate associated factor (XAP4)	32202_at	14.0	16.2	10.9	12.5
leukocystatin	3495534965 at	13.9	8.2	12.1	2.6
vav oncogene	1919_at	13.9	15.6	19.2	3.5
beta-2-adrenergic receptor	610_at	13.9	9.1	15.9	3.6
DNA from chromosome 19p13.2 cosmids R31240, R30272 and R26549 R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes	1751_g_at	13.9	17.2	10.9	23.2

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
DNA sequence from PAC 56H14-66H14 on chromosome 6q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms	40479_at	13.4	11.0	16.4	13.5
transcription factor LSF	40084_at	13.3	12.3	11.3	11.7
rap2	41318_g_at	13.2	3.3	5.9	2.8
activation (Act-2)	36674_at	12.8	7.1	12	-1.1
pM5	33414_at	12.8	10.2	8.8	8.2
CGAAT CCAAT transcription binding factor subunit gamma	404884 40466_at	12.8	18.3	18.7 16.7	14.6
CD4-related protein involved in lymphoma lymphocyte activation	36776_at	12.8	23.0	27.0	5.0
SYT Interacting interacting protein SIP	41460_at	12.7	10.7	10.3	15.7
MHC class I	34934_at	12.6	13.9	18.2	21.2
DNA dependent ATPase and helicase (ATRX)	818_s_at	12.6	7.4	13.3	10.0
bruton Brutons tyrosine kinase (BTK), alpha-D-galactosidase-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3)	36833_at	12.6	6.8	4	3.9
Natural natural killer cell BY55	33112_at	12.6	15.9	10	-2.2
leukocyte IgG receptor (Fc-gamma-R)	37200_at	12.5	9.8	9.7	-2
KIAA0080 gene	36144_at	12.4	14.3	11.8	3.0
tax1-binding protein TXBP181	499_at	12.4	11.1	17.0	6.6
gb=A1652860 A1652660	41590_at	12.3	6.3	9.7	11.3

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Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
C-terminal binding protein 2	40780_at	12.1	5.5 0.7	5.5	1.1
NuMA	33822_at	11.9	19.8 11.3	9.8 19.8	25.0
	160043_at	11.9	13.1 6.7	3.1	4.2
lymphoma proprotein convertase (LPC)	34361_at	11.7	11.7 11.4	11.7	11.7 11.1
RGP3	37637_at	11.4	9.9 2	9.9	3
gb=W26655	39045_at	11.3	11.7 5.6	11.7	6.2
KIAA0064 KIAA0226 gene	31802_at	11.3	3.8 2.4	3.8	17
KIAA0064 gene	37654_at	11.2	11.3 15.8	11.3	9.9
G9a	36200_at	11.1	11.0 9.1	11.0	6.7
Human transforming growth factor-beta type III receptor (TGF-beta)	1897_at	11.1	97.6	9	4.3
guanylate binding protein isoform 1 (GBP-2)	35735_at	11.1	29.5 23.8	29.5	6
KIAA0199 gene	37656_at	11.0	14.6 10.4	14.6	15.0
gb=AA194159	41282-a-at_s _at	10.9	10.7 11.3	10.7	17.7

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
carnitine palmitoyltransferase I type II	35936_g_at	10.9	11.8 9.1	11.8	8.8
carnitine palmitoyltransferase I type I	35228_at	10.8	14.3 11.1	14.3	7.9
Daxx	4115141161 at	10.8	15.4 10.7	15.4	13.7
B-ATF	39942_at	10.7	10.4 12	10.4	2.4
AUH	37616_at	10.7	16.0 8.6	16.0	10.5
(TAF1170 TAF1170-alpha)	37271_at	10.7	8.66 9	8.6	11.1
serine protease-like protein	37137_at	10.6	6.25 8	6.2	1.2
T-cell receptor T1-Ti rearranged gamma-chain mRNA V-J-C region	41468_at	10.6	19	25.1	9.7
PEST phosphatase interacting protein homolog (H-PIP)	34914_at	10.6	8.1	8.3	8.2
KIAA0808 protein	33316_at	10.3	4.8	5.6	1.5
Nuclear -nuclear protein, NP220	32674_at	10.3	7.5	12.1	15.3
beta-galactoside -galactoside alpha-2,6-sialyltransferase	41352_at	10.2	8.9	6.1	13.8
HREV107-like protein	35704_at	10	8.9	5.4	-1.6
adenylyl eye ase-cyclase type IX	33800_at	9.9	8.4	8.1	4.3
guanine nucleotide exchange factor mss4	38264_at	9.9	9.3	11.4	12.9
fibrinogen-like protein (pT49 protein)	39591_s_at	9.9	14	12.1	-3.1

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
XAP-5	36599 <u>38599</u> s_at	9.8	9.5	12.2	10.1
DNA from chromosome 19p13.2 cosmids R31240, R30272 and R23549 <u>R28549</u> containing the EKLF, GCDH, CRTC, and RAD23A genes	1750_at	9.7	10.4	12.0	14.8
guanine nucleotide exchange factor	33280 <u>33260</u> at	9.6	6.9	6.2	4.7
DEAD-box protein p72 (P72)	41260_at	9.4	14.0	87.2	23.5
calcium/calmodulin-dependent protein kinase II	32105_f_at	9.4	7.3	10.3	7.2
IFN-gamma	40702_at	9.3	11.7	9.4	-2.8
IL-17	36229_at	9.3	19.1	4.6	25.5
KIAA0122 gene	40070_at	9.3	4.1	10.4	5
NKG2D gene, exons 2-5	36777_at	9.3	8.7	8	12.6
alanyl-tRNA synthetase	36185_at	9.2	12.1	15.8	25.5
gb=AL080203	40451_at	9.1	13.2	10.2	11.5
gb=AA524058	34359_at	9	6.1	4.6	7.6
P-glycoprotein (PGY1)	1576_g_at	9.0	8.6	18.1	14.9
bcl-xL	34742_at	8.9	6.6	3.4	7.3
putative dienoyl <u>dienoyl</u> -CoA isomerase (ECH1) gene	32756_at	8.9	12	11.8	10.9
KIAA0245 KIAA0248 gene	40123_at	8.9	5.4	4.8	4.3
gb=AF070533	41744_at	8.8	7.8	7.7	8.7
alpha-2,3-sialyltransferase sialyltransferase (SIAT4A)	40290_f_at	8.8	7.7	10.2	10.2
ADP-ribosylation factor	36193_at	8.8	9/19 1	9.1	11.7

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=AI540958	34891_at	8.8	12.6	10.1	8.4
oligo A synthetase E	38388_at	8.8	7.8	16.8	1.2
gb=AA631972	39119_s_at	8.7	9.8	7.1	4.5
pyruvate dehydrogenase (EC 1.2.4.1) beta subunit	39160_at	8.7	4	6.2	6.2
gb=A1432401A1432401	39593_at	8.7	19.2 19.3	20.2	-6.9
gb=U51712	39698_at	8.6	9.6	3.3	3.9
glucocerebrosidase glucocerebrosidase (GCB)	32632_g_at	8.6	10.3	8.3	7.5
T cell-specific protein (RANTES)	1405_1_at	8.6	8.1	9.4	4.9
aminoacylase aminoacylase-1 (ACY1)	37713_at	8.6	9.0	5.6	9.7
multidrug resistance protein 5 (MRP5)	1933_g_at	8.4	9.4	5.4	3.4
gb=AL050259	40521_at	8.2	7.3	10.7	7.5
carboxyl methyltransferase	37736_at	8.2	9.6	6.4	10.1
gb=AA176780	40485_at	8.2	15.9	10.2	21.7
KIAA0955 protein	41100_at	8.2	8.1	11.1	10.8
gb=AL079277	41710_at	8.1	7.7	3.1	-1.7
KIAA0129 gene	33253_at	8.1	11.1	7.4	10.6
gb=AA16987AA156987	39162_at	8.0	11.1	7.3	14.8
testis testis-specific cAMP-dependent protein kinase catalytic subunit (C-beta isoform)	36215_at	7.9	5.1	5.9	7.3
KIAA0898 KIAA0898 protein	33107_at	7.8	4.5	7.9	6.1 8.1
tactile protein	34961_at	7.8	8.5	5.4	28.1
3-alkyladenine DNA glycosylase (HAAG)	37768_at	7.8	6.3	8.7	9.8

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
helicase-like protein (HLP)	37998_at	7.8	9.0	9.2	11.8
17-beta-hydroxysteroid dehydrogenase	36626_at	7.8	8.8	38.2	7.9
gb=AF035282	41679_at	7.7	6.75 7	6.8	3.8
beta2-chimaerin	33244_at	7.6	7.2	4.6	-1.5
Butyrophilin butyrophilin (BTF3)	38241_at	7.6	6.2	8.8	4.2
Protein protein kinase C-theta (PRKCT)	38949_at	7.6	6.15 1	8.8	7.5
homolog of yeast mutL (hPMS1) gene	525_g_at	7.5	8.96 9	9.0	9.1
heat shock protein (hsp 70)	1104_s_at	7.5	19.3	13.1	8.4
receptor protein 4-1BB	31540_at	7.5	7.4	6.78 7	-1.2
fibrinogen-like protein (pT49 protein)	39592_at_r_at	7.4	8.4	7.0	-1.6
RLIP76	36626_at	7.4	8.2	8.6	11.6
copper chaperone for superoxide superoxide dismutase (CCS)	38088 36068 at	7.3	7.8	10.5	9.3
TAR RNA binding protein 2 (TRBP2)	35657_at	7.3	7.3	5.5	7.3
N-myristoyltransferase N-myristoyltransferase 1	39000_at	7.3	10.0	10.0	13.8
gb=AA126515	41172_at	7.3	5.4	8.8	8.9
gb=W27519	32326_at	7.3	65 5	6.9	9.1
synaptogyrin 3	40314_at	7.2	7.4	9.7	3.4
gb=A1852521A1862521	39743_at	7.2	4.7	4.7	5.5
Human replication protein A	1382_at	7.2	4.0	4.8	6.9

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
puromycin sensitive aminopeptidase	39431_at	7.2	5.2	15.4	9.9
gb=A1014538AI014538	38623_at	7.2	7.9	7.2	9.9
gb=AF055004	34831_at	7.2	8.56 5	6.9	3.6
Endothelial Cell Growth Factor 1	1665_s_at	7.2	28.7	32.9	-11.3
gb=AL040137	41807_at	7.2	7.3	8.7	4.1
gb=AF007155	40472_at	7.1	6.6	6.9	6.7
lymphoid phosphatase LyP1	3880836808 at	7.1	3.1	5.6	2.7
Hanukah factor serine protease (HuHF)	40757_at	7.1	6.1	4.6	1.3
TM7XN1	35789_at	7.1	5	5.4	1.1
gb=AB011133	33223_at	7	6.1	4.9	2
cyclin-dependent kinase 4 (CDK4)	1942_s_at	7.0	7.5	5.4	10.2
WD repeat protein HAN11	38171_at	7.0	4.0	3.5	2.7
T cell-specific protein (RANTES)	1403_s_at	7	5.7	6.8	3.4
KIAA0067 gene	3415834189 at	7.0	7.07 9	11.8	10.4
gb=AI670100	34724_at	7.0	7.9	6.5	5.2
BRCA1, Rho7 and vat1 genes, complete cds, and lpl35-ipf35 gene	626_s_at	6.9	13.4	8.2	1.9
gb=H68340	41446_f_at	6.9	7.2	13	3.3
RasGAP-related protein (IQGAP2)	3727837276 at	6.9	4	8.1	2.7
RBP2-retinoblastoma binding protein 2	36999_at	6.9	8.5	13.3	15.9

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
KIAA0102 gene	37359_at	6.8	5.8	3.7	4.8
gb=AL050060	35840_at	6.8	17	5.9	4.5
<u>Clk2clk2</u>	646_s_at	6.8	9.5	11.5	13.8
gb=AL048308	32768_at	6.7	5.3	7.1	5.2
gb=AA877795	33854_at	6.7	7.3	9.2	5.7
KIAA1062 protein	38313_at	6.7	3.1	3.5	1.1
a-glucosidase 4I	38464_at	6.7	6	6.9	9.9
retinoblastoma	40418_at	6.7	6.8	5.1	5.2
gb=AF026402	40485 40465_at	6.7	8.2	8.9	8.3
metase (MET-1)	32264_at	6.7	4.4	3.1	1.2
axin (AXIN)	33319_at	6.6	6.3	4	4.2
adenylate kinase (AK1)	35997 36997_at	6.6	4.8	10.9	5.7
cbl-b	514_at	6.6	5.4	11.4	13.6
T-cell differentiation antigen Leu-2/T8	40599 40699_at	6.6	5.6	4.8	4.1
gb=W26892W28892	33850_at	6.5	7.8	6.5	8.9
mBA-m6A methyltransferase (MT-A70)	32246_g_at	6.5	6.7	8.5	13
1,4-alpha-glucan branching enzyme (HGBE)	32643_at	6.5	6.1	7.1	9.3
DP prostanoid receptor (PTGDR)	31782_at	6.4	6.7	3.6	4.3
interleukin 2 receptor gamma chain	1506_at	6.4	4.2	4.1	4.1
translational inhibitor protein	32173_at	6.4	5.5	4.5	4.9
gb=AI800578	34728_g_at	6.4	7.7	9.2	8.1

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
tudor repeat repeat associator associator with PCTAIRE 2	40852_at	6.4	7.0	7.7	6.8
gb=AL080111	34752_at	6.3	3.9	7.9	7.4
granulocyte colony-stimulating factor induced gene	37121_at	6.3	4.9	4.7	1.1
carboxyl terminal LIM domain protein (CLIM1)	38937 36937_s_at	6.3	6.1	4.4	-1.6
gb=AF091084	35329_at	6.3	9.1	6.9	11.4
gb=AL041683AL041663	32662_at	6.3	4.7	4.3	5.2
gb=AA160055AAI60056	40937_at	6.3	4.8	5.0	12.5
NK receptor (NKp45)(NKp46), isoform d	34040_s_at	6.3	6.3	7.4	3.6
serine/threonine protein kinase EMK	965_at	6.3	6.9	6.1	8.7
small GTP-binding protein	40889 40669_at	6.3	5.1	5.4	2.3
gb=AA576724	41648 41646_at	6.3	5.8	6.4	5.6
RING zinc finger protein (RZF)	35811_at	6.3	6	8.5	4.7
KIAA0010 gene	32044_at	6.2	7.1	6.3	7.2
TBP-associated factor (hTAFII130)	142_at	6.2	5.7	5.8	6.8
gb=AW024285	41177_at	6.2	6.3	3.7	2.6
gb=D50920	34289_f_at	6.2	6.2	4.4	7.6
GARS-AIRS-GART	38384_at	6.2	7.3	8.6	7.5
SCA2	36998_s_at	6.2	6	7.4	9.5
sigma 3B	32030_at	6.1	4.6	6.7	1.5
KIAA0386 gene	37112_at	6.1	6.3	4.1	18.1

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
nucleolar protein hNop56	34882_at	6.1	5.5	4.2	11.4
RP105	40715_at	6.0	10.1	6.0	5.2
gb=W28167	34404_at	6.0	6.3	5.4	7.9
MAP kinase kinase kinase 4 (MKK4)	36910_at	6.0	4.4	7.4	7.5
eIF4GII	33907_at	5.9	5.9	7.5	2.6
WWp2-like mRNA	33629_at	5.9	6.1	5.3	2.9
G6PD gene for glucose-6-phosphate dehydrogenase	38043_at	5.9	3.5	4.8	9.0
LTG19	32400_at	5.9	6.2	6.3	5.4
KIAA0796 protein	38113_at	5.9	4.2	5.3	3.2
interleukin 2 receptor beta chain (p70-75)	1365_at	5.9	6.5	4.8	1.1
KIAA0060 gene	34332_at	5.8	7.8	7.9	14.5
low density lipoprotein receptor gene	32855_at	5.8	10.1	5.2	28.0
Huntington's Huntingtons Disease (HD)	37767_at	5.8	4.7	4.7	3.8
monocarboxylate transporter 2 (hMCT2)	35547_at	5.8	5.1	6	14.1
DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containign containing the ELKFEKLF, GCDH, CRTG, and RAD23A genes	1753_a_at_s_at	5.8	3.1	8.3	4.6
KIAA0053 gene	38149_at	5.8	5.2	9	5
Gb=AI143868	34816_at	5.8	4.6	5.1	7.7
serine phosphatase FCP1a (FCP1)	35979_at	5.8	6.2	5.4	5.2
similar to cytoplasmic dynein dynein light chain 1	31655_at	5.7	7.7	6.06.9	3.2
KIAA1064 protein	3688036860_at	5.7	5.2	3.1	5.9

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
transactivator protein (CREB)	37535_at	5.7	5.8	8.6	10.2
Human immune interferon (IFN-gamma)	1611_s_at	5.7	5.3	4.5	-1
gb=AF052135	39391_at	5.7	8	7.6	9.6 9.7
acylphosphatase acylphosphatase, erythrocyte (CT) isoenzyme	33334_at	5.6	4.9	5.5	7.5
hRIF hRIF beta subunit (p102 protein)	33252_at	5.6	6.0	4.2	5.2
ABC transporter MOAT-C (MOAT-C)	41428_at	5.6	6.9	8.3	9.1
ras GTPase-activating-like protein (IQGAP1)	1825_at	5.6	6.2	6.1	4.2
protein tyrosine phosphatase (PTPase-alpha)	1496_at	5.6	3.8	5.2	3
retinoblastoma susceptibility	2044_s_at	5.6	4.4	5.6 5.5	2.3
KIAA0877 protein	39021_at	5.6	5.3	4.5	4.5
translocation T(4:11) of ALL-1 gene to chromosome 4	1124_at	5.5	4	7.6	6.4
osteoclast stimulating factor mRNA	467_at	5.5	4.9	4.4	4.1
kinesin-like DNA binding protein	356_at	5.5	5.1	9.2	6.5
IkB IkB kinase beta subunit	35960_at	5.5	4.1	5.4	9.3 9.9
gb=AW044624	41551_at	5.4	5	6.6	4.6
gb=AA127624	33865_at	5.4	3.8	4.6	6.5
RNA binding protein DEF-3	40869_at	5.4	6.0	6.8	6.7
Protein-protein phosphatase 2A B alpha1 regulatory subunit	178 176_at	5.4	4.4	7.8	8.4 8.1
integrin ntegrin beta-7 subunit	2019_s_at	5.4	5.9	3.8	5.3
cdc25+ homolog	1347_at	5.4	4.7	3.8	10.3

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
Ndr protein kinase	3821736217 at	5.3	4.3	7.7	7.2
KIAA0625 protein	40083_at	5.3	6.6	7.9	8
KIAA1012 protein	3800236002 at	5.3	6.5	8	8.3
protein phosphatase 2A Balphal regulatory subunit	4078840786 at	5.3	4.2	7.2	6.3
WD40 protein BING4	33250_at	5.3	4.0	3.4	5.5
serine kinase SRPK2	1213_at	5.3	3.3	7.7	2.2
interferon regulatory factor 3	371_at	5.3	4.3	5.7	5.9
nuclear localization signal containing protein deleted in Velo-Cardio-Facial syndrome (Nivef)(Nlvcf)	32745_at	5.2	4.9	4.4	4.4
gb=D45288	35310_at	5.2	3.2	3.3	2.1
gb=AI695103AI698103	35993_s_at	5.2	7.4	6.3	8.6
gb=X95808	41046_s_at	5.2	5.7	8.3	11.3
endo/exonuclease Mre11 (MRE11A)	32870_g_at	5.2	4.3	6.9 5.9	6.3
beige protein homolog homolog (chs)	35695_at	5.2	5	7.6	2.9
gb=AL049703	32212_at	5.1	5.2	4.0	6.4
leucocyte leucocyte vacuolar protein sorting	35779_at	5.1	8.4	6.3	6
programmed cell death- 2/Rp8 homolog	855_at	5.1	7.3	4.3	7.8
malate dehydrogenase precursor (MDH) mRNA, nuclear gene encoding mitochondrial protein	39001_at	5.0	4.5	4.6	5.2
gb=AL049955	34347_at	5	3.3	5.5	7

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=U37012	33132_at	5	16.8	3.4	7.2
gb=D82351	31671_at	5	3.9	4.2	3.2
uracil-DNA glycosylase	37688 37686_s_at	5.0	3.5	5.9	5.5
KIAA0011 gene	36932_at	5.0	4.5	5.8	7.8
YL-1 protein (nuclear protein with DNA-binding ability)	33873_at	5	4.2	6.7	7.1
tRNA synthetase-like protein	34291_at	5	7	6	8.2
protein kinase C-binding protein RACK7	842_at	5.0	4.9	3.8	4.6
KIAA0312 gene	34372_at	5.0	3.7	6.7	4.7
SF2p33	36099_at	4.9	4.6	3.7	5.0
gb=AB014597	39380_at	4.9	3.5	3.7	4.3
gb=R59697	35140_at	4.9	4.1	4.6	6.4
gb=U36501	37354_at	4.9	5.2	3.4	5.4
ZBP-59 protein	41465_at	4.9	3.6	5.2	5.1
ribulose-5-phosphate-epimerase	37797_at	4.9	4.0	7.2	9.2
C2f	39397 39357_at	4.9	5.1	4.9	6.6
GT335	41749_at	4.9	5	5.9	4.3
Human poly(ADP-ribose) synthetase	1287_at	4.9	6	4.4	7.5
KIAA0132 gene	35322_at	4.9	5.36 3	9.3	6.2
gb=AF052162	41176_at	4.8	4.4	3.4	1.7
class II histocompatibility antigen-like protein mRNA	34427-at_g_a t	4.8	3.1	4.0	4.0

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=AF060862	40352_at	4.8	3.9	3.3	2.6
G4 protein (G4 gene, located in the class III region of the major histocompatibility complex)	41053_at	4.8	6.1	4.7	8.2
putative mitochondrial outer membrane protein import receptor (hTOM)	34345_at	4.8	6.4	4.4	7.2
nitrilase -nitrilase1 (NIT1)	39735_at	4.8	3.8	7.5 7.6	7.1
gb=L13435	160024_at	4.8	5.7	3.1	6.7
gb=L13435	33126_at	4.8	4.1	6.5	5.8 5.6
Smg GDS-associated protein SMAP	40779_at	4.8	3.9	4.4	6.3
KIAA0854 protein	41503_at	4.7	3.4	4.3	4.2
gb=AA173896	34340_at	4.7	9.3	6.5	8
gb=AA975427	31738 31736_at	4.7	4.1	4.1	4
gb=W27939	38658 38656_s_at	4.7	3.6	3.9	4.3
Human translational initiation factor (eIF-2)	1154_at	4.7	5.3	4	2.9
NADP-dependent isocitrate dehydrogenase (IDH)	39023_at	4.7	8.9	12.6	5.8
heterochromatin heterochromatin protein p25	37304_at	4.7	4.6	5.7	5.7
mRNA -mRNA for small GTP-binding protein	37466_at	4.7	6.4	5.7 5.4	6.3
methyl-CpG-binding protein	34355_at	4.7	4.4	4.6	5.8 5.6
mRNA for imogen	40072_at	4.6	4.2	4.9	6.6
transcription factor NFATx4	40823_s_at	4.6	4.5	3.1	3.9
nexin 1 (SNX1)	36583_at	4.6	8.5	12.3	9.8

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=U79282	32069 <u>32059</u> at	4.6	4.0	5.2	4.2
gb=A1760162A1760162	41058_g_at	4.6	7.3	6.0	8.6
gb=AA224832	39120_at	4.6	5.7	9.3	9.4
KIAA0648 protein	34353_at	4.6	3.1	5.1	6.4
gb=AB007889	37383 <u>37363</u> at	4.6	4	5.5	1.3
homolog of yeast mutL (hPM31)(hPMS1)	41481 <u>41461</u> at	4.6	3.6	4.5	5.5
UDP-glucose dehydrogenase (UGDH)	35214_at	4.6	3.9	4	6.4
KIAA0560 protein	41712_at	4.5	4.2	5.3	6.8
gb=AL060390AL050390	31852_at	4.5	3.8	3.7	3.6
similar to Drosophila Drosophila ash2	35804_at	4.5	5.8	8.5 <u>6.5</u>	5.7
gb=A1928387A1928387	33225_at	4.5	4.5	4.8 <u>4.6</u>	5.4
SCM-1beta precursor	31498 <u>31496</u> g_at	4.5	25.9	8.2	5.7
putative glucosyltransferase	32051_at	4.5	4.6	3	5.7
retinoic acid receptor responder 3 (RARRES3)	33236_at	4.5	4.2	4.6	1.6
KIAA0350 gene	34661_at	4.5	5.4	3	5.1
CACCC box-binding protein	41466_s_at	4.5	3.1	4.3	3.9
mutator gene (hMSH2)	860_at	4.5	5.0	3.8	13.1
tyrosylprotein sulfotransferase-2	35172_at	4.5	5	4.2	3
DNA polymerase gamma	1014_at	4.4	3.5	4.6	4
DORA protein	34946_at	4.4	14.8	13.2	-3.0

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=A1246728A1246726	37046_at	4.4	4.3	3.8	5.9
galactokinase (GK2)	37825_at	4.4	3.7	4.7	3.4
gb=AW051579	33191_at	4.4	4.2	3.6	4.5
Heat shock-shock protein 70 testis variant	40656_at	4.4	5.0	4.1	5.9
gb=AA142942	33399_at	4.4	5.3	4.3	4.6
gb=U26710	35832 35632_at	4.4	3.1	5.0 5.4	7.4
stress-activated protein kinase 4	33245_at	4.4	3.8	4.0	3.3
ST15	35234_at	4.3	3.3	3.9	6.2
villin-like protein	37123_at	4.3	3.4	4.1	3.6
gb=U79255U79256	37677 37577_at	4.3	3.2	4.7	2.5
gb=L13744	35975_at	4.3	3.4	5.9	8.3
gb=AL049701	34446_at	4.3	3.3	5.1	2
FIP2 alternatively translated	41743-1 at_i_at	4.3	4.3	4.9	4.3
NF-AT4c	40822_at	4.3	4.1	4.5	3.9
putative poly(ADP-ribosyl) transferase (PARPL)	37303_at	4.3	4.4	4.9	4.6
KIAA0373 gene	38135_at	4.3	3.8	5.4	5.8
gb=W26640	35357_at	4.3	4	3.4	9.3
SCM-1beta precursor	31495_at	4.2	31.5	8.8	8.1
gb=D87077	38892_at	4.2	3.9	5.1	4.1
mitochondrial RNA polymerase	40232_at	4.2	3.5	5.3	4.7
gb=AA780049	40615_at	4.2	4.1	5.4	3.2

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=AA905543	38620_at	4.2	5.0	<u>4.84.6</u>	2.7
(AF1q)	36941_at	4.2	4.0	5.1	11.1
KIAA0018 gene	38658 36658_at	4.2	5.9	3.1	4.7
platelet activating receptor homolog (H963)	31919_at	4.2	3.4	13.9	9.9
SET-binding protein (IEF-SP 3521)(SEB)	34990_at	4.2	4.3	6.2	1.3
transformation sensitive protein (IEF SSP 3521)	207_at	4.2	8.3	3.6	6.6
protein-tyrosine phosphatase	14801 1460_g_at	4.2	4.2	6.4	4.1
(GalT3 (beta3-Galactosyltransferase))	35944_at	4.1	3.9	5.4	3.5
Arp2/3 protein complex subunit p16-Arc (Arc15)(Arc16)	38392_at	4.1	3.8	3.7	3.9
nuclear receptor co-repressor N-CoR	39722_at	4.1	5.1	6.1	4.2
gb=AA808981AA808961	38287_at	4.1	5.2	4.4	2.3
transcription factor ISGF-3	AFFX-HUMISGF 3A/M9793 5_3_at	4.1	5.2	7.3	2.7
Jak2 kinase	37468_at	4.1	6.15. 1	5.5	3.5
transcription factor ISGF-3	AFFX-HUMISGF 3A/M9793 5 MA at	4.1	3.9	6.9	1
24p21-activated protein kinase (Pak1)	1558_g_at	4.1	6.9	6.15.1	-1.5
gb=D79985	33889_s_at	4.1	3.8	4.6	7.1
gb=AB002347	39797_at	4.1	4.5	7.1	8.1

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=D79998	34858_at	4.1	3.8	4.7	8.8
short form transcription factor C-MAF (c-maf)	415064 1505_r_at	4.1	4.8	3.1	2.6
gb=AW051579	33192_g_at	4.1	5.2	5.7	5.8
lycosylphosphatidyl inositol-anchored protein GPI-80	34498_at	4.1	3.7	11.2	1.6
DNA helicase (RECQL)	34684_at	4.1	5.2	7	8.6
KIAA0838 protein	34719_at	4.1	4	6.2	7.4
SKAP55	38862_at	4.1	3.3	4.3	2.2
Sel-1 like mRNA	40689_at	4	3.4	3.6	3.4
c-myc binding protein	1904_at	4	5.3	3.4	4.1
T-cell receptor alpha chain C region	432_s_at	4	5.1	3	4.8
calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17)	33908_at	4	5.5	3.9	3.5
uridine diphosphoglucose diphosphoglucose pyrophosphorylase	37373_at	4	3.6	3.7	3.7
SH2D1A	38147_at	4	3.4	4.4	3.9
gb=AL035295AL035296	37119_at	4.0	3.4	6.4	5.3
gb=AF070595	38170_at	4.0	3.0	4.2	6.5
gb=H05692	35283_at	3.9	4.0	5.4	5.4
gb=AI540318	41234_at	3.9	3.5	5.5	3.4
gb=X79882	38064_at	3.9	4.7	3.3	2.3
GAP binding protein p62dok (DOK)	815_at	3.9	5.3	6.9	3.7
OPA-containing protein	40998_at	3.9	4	4.1	5.4
myogenic determining factor 3 (MYOD1)	33482_at	3.9	4.0	4.2	4.9

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=AA293354AA203354	38981_at	3.9	6.2	3.7	5.7
gb=AF006083	35271_at	3.9	3.4	3.1	3.2
ICAM-2	38454_g_at	3.9	6.4	3	5.7
protein-tyrosine phosphatase	1459_at	3.9	3.2	5.9	3.7
T -lymphocyte specific protein tyrosine kinase p56lck (lck) abberant mRNA	33238_at	3.9	3.6	3.7	4.7
zinc finger protein	39261_at	3.9	4.0	6.7	7.4
KIAA0097 gene	37293_at	3.8	3.4	5.4	4.3
cytosolic acetoacetyl-coenzyme A thiolase	34790_at	3.8	3.1	3.2	6.8
NF-AT4c	250_at	3.8	3	4	2.7
gb=X77744	32883_at	3.8	4	6.1	5.4
gb=Y08614	37729_at	3.8	3.9	4.5	3.8
transcription factor WSTF	32261_at	3.8	4.4	5	5.5
TATA-binding protein mRNA	41441_at	3.8	3.2	4.6	7.3
KIAA0543 protein	41077_at	3.8	4.6	5.5	12.7
lymphocyte-specific protein tyrosine kinase (lck)	2059_s_at	3.7	3.9	4.1	4.7
CHD5 protein	32777_at	3.7	3.3	6.7	5.4
KIAA0549	4008440064_at	3.7	4	3.3	4.9
leukemia associated gene 1	33791_at	3.7	5.4	3.1	3.9
DM33Diff33	37007_at	3.7	3.9	4.6	5.6
branched chain alpha-ketoacid dehydrogenasekinase precursor	32828_at	3.7	3.2	7.6	2.9

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
gb=AL022398	40720_at	3.7	3.63 8	3.1	5.4
KIAA0748 KIAA0746 protein	41585_at	3.7	3.5	5.5	3.6
gb=AL050018	46875 36875_at	3.7	5.2	3.2	4.8
gb=D25538	40585_at	3.7	4.3	3.8	1.9
gb=X84908	37392_at	3.7	3.9	5.9	2.9
/gb=X70478X70476	36877 36677_at	3.6	3.8	4.8	4.4
Interleukin1 interleukin 1-beta converting enzyme isoform beta (IL1BCE)	39320_at	3.6	3.16 6	3.1	-1.8
Rad50	1533_at	3.6	3.73 4	3.7	3.6
snRNA activating protein complex 190kD subunit (SNAP190)	35092_at	3.6	3.96 6	3.9	6.4
gb=AI655015	39932_at	3.6	5.6 8	5	6.2
TGF-beta activated kinase 1a	36905_at	3.6	5.13 6	5.1	7
TAFII20	802_at	3.6	5.14 0	5.1	4.9
gb=AA203246	41821_at	3.6	4.84 1	4.8	4.2
KIAA0039 gene	37646_at	3.6	5.13 0	5.1	3.2

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
KIAA0494	41830_at	3.5	3.43 8	3.4	4.3
gb=AI547262	33875_at	3.5	3.33 1	3.3	2
gb=AC002310	40905_at	3.5	7.54 0	7.5	4.0
MHC class III HSP70-2 gene (HLA)	31692_at	3.5	5.18 2	5.1	4.3
T-cell surface antigen CD2 (T11)	40738_at	3.5	4.2	4.2	3.5
tob family	39286_at	3.5	5.93 3	5.9	5.8
phosphoribosypyrophosphate phosphoribosypyrophosphate synthetase-associated protein 39	37338_at	3.5	4.34 6	4.3	6.9
P-selectin glycoprotein ligand (SELPLG)	37541_at	3.5	3.13 2	3.1	3.2
leupaxin	36062_at	3.5	4.73 4	4.7	5.5
KIAA0992 protein	41191_at	3.5	3.6	6.5	-1.5
gb=W22296	36957_at	3.4	3.1	3.4	3
protoporphyrinogen protoporphyrinogen oxidase	37098_at	3.4	3.7	4.2	8.2
prolyl oligopeptidase	37950_at	3.4	3.6	4.7	2.4
Toll/interleukin-1 receptor-like protein 3 (TILS)(TIL3)	34473_at	3.4	4.0	7.2	2.4
class-I class-I MHC-restricted T cell associated molecule (CRTAM)	36389_at	3.3	11.8	9.4	12.5

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)

Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
meningioma-expressed antigen 6 (MEA6)	41615_at	3.3	4.3	5.4	6.6
HMED7 hMed7 (MED7)	36648_at	3.3	3.1	5.1	6.9
acetyl-coenzyme A transporter	346663 4668_at	3.3	3.1	4.4	3.7
KIAA0241 gene	39761_at	3.3	4.8	7.1	7.7
gb= U00948 U00946	32185_at	3.3	3.6	4.8 4.6	3.4
gb=X53390	38794_at	3.3	4	3.2	6.1
Kruppel-type zinc finger protein	35588_at	3.3	3.3	6.5	11.8
gb=AL050159	38717_at	3.3	5.5	4.2	-4.7
protein-tyrosine phosphatase 1C	794_at	3.3	5.4	3.23 3	1.1
DAP-kinase mRNA	40049_at	3.3	5.8	9.4	-2.1
KIAA1105 protein	33457_at	3.3	4.8	5.2	5.4
son-a	39097_at	3.3	3.5	4	4.6
neutral amino acid transporter B mRNA	411784 1778_at	3.3	4.2	3.4	2.8
candidate tumor suppressor gene 21 protein isoform \pm I mRNA	40498_g_at	3.2	3	3.63 3.5	2.3
KIAA0453 protein	32743_at	3.2	3.0	4.54 4.6	6.6
gb= AL060133 AL080133	41815_at	3.2	4.3	5.5	4.7
DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes	41184 _at_s_at	3.2	3.5	3	2.2
2,4-dienoyl-CoA reductase gene	38104_at	3.2	4.8	3.4	3.3
gb=AF055024	31875_at	3.2	3.3	4.4	4.9
KIAA0088 KIAA0068 gene	37306_at	3.2	7.9	11.6	-1.7

Table 2. Genes upregulated in LGL1, LGL2 and LGL3/RA (Affymetrix U 95)					
Gene Name	Accession No.	LGL1	LGL2	LGL3/RA	CD8+
		(Fold increase compared to Normal PBMC)			
mitochondrial 3-oxoacyl-CoA thiolase	41530_at	3.2	4.2	3.2	2.5
replication protein A 70kDa	38481_at	3.2	3.2	3.1	4.6
Human Interferon-gamma induced protein (IFI 16) gene	1456_s_at	3.1	3.63 5	6	3.1
VHL binding protein-1 (VBP-1)	171_at	3.1	3.6	3	4.64 5
butyrophilin (BTF5)	32629_f_at	3.1	3.6	5.35 2	3
gb=A1966201A1986201	35787_at	3.1	4.3	5.1	7.1
gb=AL050275	39115_at	3.1	3.7	4.4	8.1
gb=AI478147	4065340853 at	3.1	4.1	4.8	1.7
gb=AB028960	40829_at	3	6.7	6.7	7.5
gb=AL049435	38510_at	3.0	4.5	9.0	1.2
gb=AL080115	39442_at	3	3.7	6.3	4.6
Human phosphatase 2A	924_s_at	3	3.8	3.2	5
WNT7a	3578336763 at	3	4.5	4.4	10.0
Skeletal -skeletal muscle abundant protein	32655_s_at	3.0	3.2	6.0	7.7
Gb=R59608R59606	41302_at	3	3.4	3.9	3.5
Gbbg=AF070590	40760_at	3.0	3.7	4.1	2.1
Phosphatidylinositol-4-phosphate 5-kinase type II beta	35741_at	3	3.8	3.9	5.4
KIAA0541 protein	41430_at	3	3.4	4.6	3.7
FIP2 alternatively translated	41742_s_at	3	3	3.3	3.2

Table 3. Genes that are down-regulated in LGL leukemia patients when compared to normal (Affymetrix U 95)

Name of the Gene	Accession No.	LGL 1	LGL 2	LGL3/RA
1. KIAA0508	33581 <u>33591</u> _at	-2.8	-24.8	-23.7
2. retinal short-chain dehydrogenase/reductase retSDR1	40782_at	-1.4	-17.1	-10
3. KIAA0414	41695_at	-2.7	-13.1	-8.6
4. hypothetical protein FLJ10097	40916_at	-1.3	-10.6 <u>10.5</u>	-8.6
5. KIAA0552	38248_at	1.9	-9.7	-11.7
6. integrin alpha 6 subunit	39753_at	-2.1	-9.4	-5.3
7. KIAA0172	37225_at	-2.2	-9.1	-8.6
8. two-handed zinc finger protein ZEB	33440_at	1.5	-7.9	-8.0
9. sterol-C5-desaturase	33421_s_at	-2.4	-7.6	-10.0
10. nuclear factor RIP140	40088_at	-2.2	-6.9	-4.6
11. SCML2 protein	38518_at	-2.1	-5.8	-5.3
12. receptor protein-tyrosine kinase (HEK8)	1606_at	3.5	-5.5	-4.8
13. hSGT1	33746_at	-2.9	-5.5	-5.4
14. gb=AL080144	35672_at	-2.4	-5	-7
15. Dr1-associated corepressor (DRP1)(DRAP1)	39077_at	-1	-4.9	-14.7
16. collagen binding protein 2	39166_s_at	-2.5	-4.7	-7.4
17. CD44 isoform RC (CD44)	31472_at_s_at	-2.3	-4.6	-4.6
18. USF2	38324_at	2.5	-4.5	-5.0
19. G protein-coupled receptor (EBI 1) gene exon 3	1097_s_at	3	-4.1	-5.4
20. serine/threonine kinase receptor-2-3 (SKR2-3)	34055_at	-2.2	-4.0	-3.9
21. gb=AC002073	36231_at	-2.2	-4	-12.8
22. nel-related protein 2	32598_at	4.1	-3.9	-5.3
23. transducin-like enhancer protein (TLE3)	38234_at	-2.4	-3.9	-3.2
24. DNA binding protein (SATB1)	38899 <u>36899</u> _at	1.5	-3.8	-4.7
25. KIAA0443	37446_at	1.7	-3.8	-4.8
26. HSPNP	430_at	-1.2	-3.7	-3

27. <u>GBgb=AF052160</u>	<u>34962_at</u>	<u>-1.7</u>	<u>-3.7</u>	<u>-9.6</u>
28. LIM protein SLIMMER	<u>32542_at</u>	<u>-1.1</u>	<u>-3.7</u>	<u>-4.8</u>
29. calponin	<u>40953_at</u>	<u>2.9</u>	<u>-3.7</u>	<u>-3.6</u>
30. KIAA0346	<u>41386_i_at</u>	<u>-2.2</u>	<u>-3.7</u>	<u>-4.1</u>
31. nuclear factor kappa-B DNA binding subunit (NF-kappa-B)	<u>1378_g_at</u>	<u>-2.3</u>	<u>-3.4</u>	<u>-4.1</u>
32. You paraneoplastic antigen (CDR2)	<u>36190_at</u>	<u>-1.2</u>	<u>-3.3</u>	<u>-5.8</u>
33. cell surface glycoprotein CD44 (CD44) gene, 3 end of long tailed isoform	<u>1125_s_at</u>	<u>-2.7</u>	<u>-3.1</u>	<u>-3.4</u>
34. Death Receptor 3 (DR-3, WSL-S1, Apo-3)	<u>41189_at</u>	<u>2.3</u>	<u>-3</u>	<u>-3.8</u>
35. gb=AL049365	<u>34788_at</u>	<u>1.2</u>	<u>-3</u>	<u>-7.6</u>